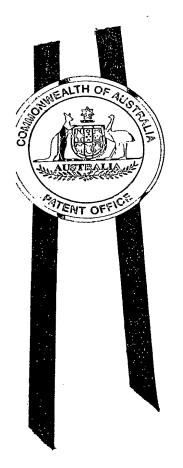


Patent Office Canberra

I, LEANNE MYNOTT, MANAGER EXAMINATION SUPPORT AND SALES hereby certify that annexed is a true copy of the Provisional specification in connection with Application No. 2003906477 for a patent by AGRICULTURE VICTORIA SERVICES PTY LTD as filed on 24 November 2003.



WITNESS my hand this Eighth day of December 2004

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LEANNE MYNOTT

MANAGER EXAMINATION SUPPORT
AND SALES

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P/00/009 Regulation 3.2

AUSTRALIA

Patents Act 1990

PROVISIONAL SPECIFICATION

Invention Title:

Modification of plant response to freezing and low temperature stress

The invention is described in the following statement:

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MODIFICATION OF PLANT RESPONSE TO FREEZING AND LOW TEMPERATURE STRESS

The present invention relates to nucleic acids or nucleic acid fragments encoding amino acid sequences for ice recrystalisation inhibition proteins in plants, and the use thereof for the modification of plant response to freezing and/or low temperature stress.

Plants have evolved a range of physiological and biochemical responses to freezing and low temperature stress. In plant species that are tolerant of freezing stress, exposure to lowering temperatures is accompanied by the accumulation of a characteristic set of proteins, called 'antifreeze proteins' (AFPs). Some AFPs act to depress the freezing point temperature allowing the plant to supercool. A class of AFPs, the ice recrystallisation inhibition proteins (IRIPs), confer freezing tolerance by inhibiting ice crystal growth, promoting the formation of small ice crystals in preference to large ice crystals that puncture membranes and disrupt the structure of macromolecular complexes. IRIP activity has been identified in extracts from a limited number of plant species, and the nucleotide sequence of one such IRIP from Lolium perenne has been reported.

As nucleic acid sequence encoding an IRIP has been isolated from only one species of plant, there is a need for materials useful in modifying the tolerance of freezing and low temperature stress, in a wide range of plants, and for methods for their use.

It is an object of the present invention to overcome, or at least alleviate, one or more of the difficulties or deficiencies associated with the prior art.

In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding IRIPs from a Deschampsia species, preferably Antarctic hair-grass, *Deschampsia Antarctica*, or functionally active fragments or variants thereof.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of

proteins which are related to IRIP or functionally active fragments or variants thereof. Such proteins are referred to herein as IRIP-like.

The individual or simultaneous enhancement or otherwise manipulation of IRIP or like gene activities in plants may enhance or otherwise alter the freezing and/or low temperature tolerance of plants.

The modification of plant freezing and/or low temperature tolerance based on the individual or simultaneous enhancement or otherwise manipulation of IRIP or like gene activities in plants has significant consequences for a range of applications in plant production and plant protection. For example, it has applications in increasing the range and productivity of plants.

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Methods for the modification of plant freezing and/or low temperature tolerance may facilitate the production of, for example, plants with enhanced tolerance of freezing and/or low temperature stress.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an IRIP or IRIP-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 5, 6, 8, 9, 11, 13, 14 and 16 hereto; (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living plant is not isolated, but the same nucleic acid or polypeptide separated from some or all of

the coexisting materials in the natural system, is isolated. Such nucleic acids could be part of a vector and/or such nucleic acids could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment.

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Such nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acid fragments, the sequences (and thus their corresponding nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

The term "purified" means that the nucleic acid or polypeptide is: substantially free of other nucleic acids or polypeptides. 15

By "functionally active" in respect of a nucleic acid it is meant that the fragment or variant (such as an analogue, derivative or mutant) is capable of modifying the tolerance of freezing and/or low temperature stress in a plant. Such variants include naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the relevant part of the above mentioned sequence, more preferably at least approximately 90% identity, most preferably at least approximately 95% identity. Such functionally 25 active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 30 nucleotides, more preferably at least 45 nucleotides, most preferably at least 60 nucleotides.

By "functionally active" in respect of a polypeptide is meant that the fragment or variant has one or more of the biological properties of an IRIP or IRIP-like protein. Additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 60% identity to the relevant part of the above mentioned sequence, more preferably at least approximately 80% identity, most preferably at least approximately 90% identity. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

The term "construct" as used herein refers to an artificially assembled or isolated nucleic acid molecule which includes the gene of interest. In general a construct may include the gene or genes of interest, a marker gene which in some cases can also be the gene of interest and appropriate regulatory sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes vectors but should not be seen as being limited thereto.

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The term "vector" as used herein encompasses both cloning and expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

By "operatively linked" is meant that said regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

By "an effective amount" it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

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Genes encoding other IRIP or IRIP-like proteins for modifying the tolerance of plants to freezing and/or low temperature stress, either as cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan, such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available in vitro transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in protocols to amplify longer nucleic acid fragments encoding homologous genes from DNA or RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence

may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol [Frohman et al. (1988) Proc. Natl. Acad Sci. USA 85:8998, the entire disclosure of which is incorporated herein by reference] to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated [Ohara et al. (1989) Proc. Nati. Acad Sci USA 86:5673; Loh et al. (1989) Science 243:217, the entire disclosures of which are incorporated herein by reference]. Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a second aspect of the present invention there is provided a substantially purified or isolated IRIP or IRIP-like polypeptide from a Deschampsia species, preferably from Antarctic hair-grass, *Deschampsia Antarctica*; and functionally active fragments and variants thereof.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated IRIP or IRIP-like polypeptide includes an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 4, 7, 10, 12 and 15 hereto and functionally active fragments and variants thereof.

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In a further embodiment of this aspect of the invention, there is provided a polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing polypeptides are well known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins comprising the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in genotype are essential in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a 5 specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide sequence information including single nucleotide polymorphisms (SNP's), variations in single nucleotides between allelic forms of such nucleotide sequence, can be used as perfect markers or candidate genes for the given trait.

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Applicants have identified a number of SNP's of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 11 and 14.

Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid fragment shown in Figures 1 to 16 hereto, or complements or sequences antisense thereto.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention 25 including a single nucleotide polymorphism (SNP), said method including sequencing nucleic acid fragments from a nucleic acid library.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid fragments may be isolated from recombinant plasmids or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of nucleic acids or nucleic acid fragments of the present invention including SNP's, and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment according to the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in grasses and cereals. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers in forage and turf grass improvement, e.g. tagging QTLs for disease resistance, insect resistance, nematode resistance. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in grasses and cereals.

In a still further aspect of the present invention there is provided a construct including a nucleic acid or nucleic acid fragment according to the present invention.

In a still further aspect of the present invention there is provided a vector including a nucleic acid or nucleic acid fragment according to the present

invention.

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In a preferred embodiment of this aspect of the invention, the vector may include a regulatory element such as a promoter, a nucleic acid or nucleic acid fragment according to the present invention and a terminator; said regulatory element, nucleic acid or nucleic acid fragment and terminator being operatively linked.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable, or integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

20 which may be employed in the constructs and vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable promoters include but are not limited to the constitutive Cauliflower Mosaic Virus 35S (CaMV 35S) promoter and derivatives thereof, the maize Ubiquitin promoter, the rice Actin promoter, and the tissue-specific Arabidopsis small subunit (ASSU) promoter.

A variety of terminators which may be employed in the vectors and constructs of the present invention are also well known to those skilled in the art.

The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (nos), the octopine synthase (ocs) and the rbcS genes.

The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (ori), multiple cloning sites, recognition sites for recombination events, spacer 10 sequences, enhancers, introns (such as the maize Ubiquitin Ubi intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (npt2) gene, the hygromycin phosphotransferase (hph) gene, the phosphinothricin acetyltransferase (bar or pat) gene and the gentamycin acetyl transferase (aaacC1) gene], and reporter genes (such as beta-glucuronidase 15 (GUS) gene (gusA) and green fluorescent proptein (gfp)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, visual examination including microscopic examination of fluorescence emitted by gfp, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or 25 nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

The constructs and vectors of the present invention may be incorporated

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into a variety of plants, including monocotyledons (such as grasses from the genera *Deschampsia*, *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as arabidopsis, tobacco, white clover, red clover, subterranean clover, alfalfa, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms.

Techniques for incorporating the constructs and vectors of the present invention into plant cells (for example by transduction, transfection or transformation) are well known to those skilled in the art. Such techniques include 10 Agrobacterium-mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

15 Cells incorporating the constructs and vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, a vector of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable species, including monocotyledons, dicotyledons and gymnosperms.

The present invention also provides a plant, plant seed or other plant part, or a plant extract, derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract, derived from a plant of the present invention.

In a further aspect of the present invention there is provided a method of modifying tolerance of freezing and/or low temperature stress in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

Using the methods and materials of the present invention, the tolerance of freezing and/or low temperature stress in a plant may be increased or decreased or otherwise modified. For example, the tolerance of freezing and/or low temperature stress may be increased or otherwise altered. They may be increased, for example, by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention. They may be decreased, for example, by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

20 In the Figures

Figure 1 shows the nucleotide sequence of DalRIPa.

Figure 2 shows the deduced amino acid sequence of DalRIPa.

Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence DaIRIPb.

25 Figure 4 shows the deduced amino acid sequence of DalRIPb.

Figure 5 shows the consensus contig nucleotide sequence of DalRIPb.

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence DalRIPc.

Figure 7 shows the deduced amino acid sequence of DalRIPc.

Figure 8 shows the consensus nucleotide sequence of DalRIPc.

5 Figure 9 shows the nucleotide sequence of DalRIPd.

Figure 10 shows the deduced amino acid sequence of DalRIPd.

Figure 11 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence DalRIPe.

Figure 12 shows the deduced amino acid sequence of DalRIPe.

10 Figure 13 shows the consensus contig nucleotide sequence of DalRIPe.

Figure 14 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence DalRIPf.

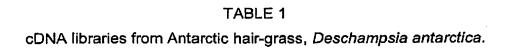
Figure 15 shows the deduced amino acid sequence of DalRIPf.

Figure 16 shows the consensus contig nucleotide sequence of DaIRIPf.

15 EXAMPLE 1

Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for IRIPs from from Antarctic hair-grass, Deschampsia antarctica.

cDNA librarires representing mRNAs from various organs and tissues from 20 Antarctic hair-grass, *Deschampsia antarctica* were prepared. The characteristics of the libraries are described below (Table 1).



Library	Organ/Tissue
05Da	Aerial parts grown at 4°C
08Da	Roots grown at -15°C
09Da	Roots transferred from -15°C to 25°C for 24 h
10Da	Aerial parts transferred from -15°C to 25°C for 24 h
11Da	Aerial parts grown at -15°C
12Da	Roots grown at -15°C
15Da	Roots grown at 4°C
16Da	Aerial parts grown at 4°C
17Da	Roots transferred from 25°C to 0°C for 48 h
18Da	Aerial parts transferred from -15°C to 0°C for 48 h
19Da	Aerial parts transferred from 25°C to 0°C for 48 h, then to -15°C for 48 h

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, 10 USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into Escherichia coli Epicurian coli XL10-Gold 15 ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

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Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The

Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New 5 England Biolabs), followed by transfection into E. coli DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser. 15

EXAMPLE 2

DNA sequence analyses

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The cDNA clones encoding IRIPs were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) J. Mol. Biol. 215:403-20 410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the eBioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) Nature Genetics 3:266-272) provided by the NCBI.

The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to a multiple alignment using the CLUSTALw algorithm, and to generate a consensus contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT protein sequence database using the BLASTx algorithm to confirm the initial identification.

Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

15 Agriculture Victoria Services Pty Ltd
By their Registered Patent Attorneys
Freehills Carter Smith Beadle

24 November 2003

		* 20 * 40 * 60	
DaIRIPa	:	GAGCTTCAACACTGTCGTAATTGGGAGTGACAATATCATAACCGGTAGCAAGCA	60
DaIRIPa	:	* 80 * 100 * 120 ATCTGGGAGGAAACATATCGTAACTGATAACAACAACAAGTATCCGGGAATGACAATAA :	120
DaIRIPa	:	* 140 * 160 * 180 TGTATCCGGGAGCTTCCACACCGTATCCGGGAGCAACACCCGTATCCGGGAGCAACAA	180
DaIRIPa	:	* 200 * 220 * 240 TACCGTTTCCGGGAGCAACCATGTCGTGTCTGGGAGCAACAAAGTCGTGACAGGAGGTTA	240
DaIRIPa	:	* 260 * 280 * 300 ATTATGTGTCAGGATTGTCTCCACCTGAGCTCACCCCTTGTCCAAATTGAGTCTA	:300
DaIRIPa	:	* 320 * 340 * 360 GCTCACAATCAGTTGGTGGGGCCAATCGCGGCATGTAACTTCATGGATGG	: 360
DaIRIPa	;	* 380 * 400 * ATTTTCCCACTTTAAATAAATTTGCCTCGTGGATGTCTAAAAAAAA	

* 20 * 40 * 60

DaIRIPa : SFNTVVIGSDNIITGSKHVVSGRKHIVTDNNNKVSGNDNNVSGSFHTVSGSHNTVSGSNN : 60

DaIRIPa : TVSGSNHVVSGSNKVVTGG : 79

		*	20	*	40	*	60		
DaIRIPb1	•	2		AACACAACAC	ACTATTACGT	GCAGTCACGAC	AATGCCGT	:	40
DaIRIPb2	•	TCAGCAACGTTGN	GACTGGA	RETACATICAC	ACTIONACGTO	GGAGTGACGAC	AATGCCGT	:	60
DaIRIPb3	:	ACAGCAACGGTGT	GACTGGA	AACACAACAC	ACTATTACGTG	GGAGTGACGAC	AATGCCGT	:	60
DaIRIPb4	:	ACAGCAACGTTGT	GACTGGA	ACACAACAC	ACTATTACGTO	GGAGTGACGAC	AATGCCGT	:	60
DOTIVEDA	٠		CC						
		*	80	*	100	*	120		
DaIRIPb1		AAGTGGTAGCAAG		TATICTCCCAC		TAACTGGCGAC		:	100
DalRIPb2	•	AAGTGGTEECAAG	CATGICG	TATETGEAC	CCACCATGTCG	TAACTGGCGAC	AACAATGO	:	120
DaIRIPb3	•	AAGTGGTAGCAAG	CATGICG CATGTCG	TAT <u>R</u> IGEORC	CCACCATGTCG	TAACTGGCGAC	DACAATGO	:	120
	:	AAGTGGTAGCAAG	CAIGICG CATCTCC	INICIGGONC TATOTOTOTO	いというととなれては、	TAACTOCCCA TAACTCCCCCA	CAACAATICC	:	120
DaIRIPb4	•	AAGIGGIAGCAAG	CMICHE	INICIONA		Trinciación		•	
			140	•	160	*	180		
D- TDTDL1		CCTAACAACGAAC		CCCTATOCCC		CCCTACCTICCC			160
DaIRIPb1	;	CGTAACAAGGAAC						:	180
DaIRIPb2	:	CGTAACAAGGAAC						:	180
DaIRIPb3	:	CGTAACAAGGAAC	CACAAIA	CCGIAICCGC	CAGCCATAATA	CCGTACCTGGG	ACCCATIAN	:	180
DaIRIPb4	:	CGIMACAAGGAMC	CYCVATA	CCGTVICCGG	GVGCCXIIVIII	CCGINCCIGGE	MOCCATIVE	•	100
		_	000		220	•	240		
		m> 000m2 mamaaa	200	* ************************************		7 m 7 CCC to 7 to Cu		:	220
DaIRIPb1	:	TACCGTATCTGGG	AGCCACA	ATACCGTATC	. PGGGAGCCACA	AINCEGIAICI AMA CCCMA TCT	CCAACCAT	:	240
DaIRIPb2	:	TACCGTATCTGGG	AGCCACA	ATACCGIATC	. IGGGAGCCACA	ATACCGTATCT	GGAAGCISI	•	240
DaIRIPb3	:	TACCGTATCTGGG	AGCCACA	ATACCGIATC	TGGGAGCCACA	ATACCOTATCI	CCAACCAA		
DaIRIPb4	:	TACCGTATCTGGG	AGCCACA	ATACCGTATC	TGGGAGCCACA	ATACCGTATCT	GGAAGCAA	•	240
		•	0.50		280		300		
		CCACATCGTATCT	260	7 C 7 7 7 CTCCT		~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~			280
DaIRIPb1	:	ECACATEGIATET ECACATEGIATET	GGGAACA	ACAAAGICGI	GALAIGAGGII Cacameacem	AAIGAICIIIA AATCATCTTTA	CTCCATTC	:	300
DaIRIPb2	:	CCACATCGTATCT	GGG/V4CA	ACMMIGICGI ACAMIGICGI	CACATGAGGII	AAIGAICIII AATGAICTTTA	GTCGATTC	:	
DaIRIPb3	:	CCACATCGTATCT	GGGAACA	ACMMGICGI ACAMMGICGI	CALCATORACCET	AAIGAICIIIA AATGATCTTTA	GTGGATTG	·	300
DaIRIPb4	:	CCACATCGTATCT	UGGAACA	ACAAGICGI	GACATGAGG11	MAIGHICITIA	011001110	•	500
			320		340	*	360		
		TTTCCATCTTCCC		ריריזירי א ידירידיידיר		A A TA A CTCTAC			340
DaIRIPb1	:	TTTCCATCTTCCC	TANCOAA	COTONTO II	A I G I CCMMOC I	~~1 ~~G1G1~~C	CTCACAGT		360
DaIRIPb2 DaIRIPb3	:	TTTCCATCTTCCC	TMLCGMA	CCTCATGTTC	TODA ACCT	AATAAGTGTAC AATAAGTGTAC	CTCACAGT	:	360
DaIRIPD3	•	TTTCCATCTTCCC	TMXCGMX	CCTCATGTTC	'ATCTCCAACCT	AATAAGTGTAC	CTCACAGT	:	
Darkibba	•	TITCCATCLICCC	IAACGAA	CCICHIGIIC	ATOTOCHOU	PERTURSOT OF FIG.	CT CHC. TO.	•	
		•	380	*	400	*	420		
DaIRIPb1	_	CACTTGGTGGGGC				AGCATCATTT			400
Dalkipbi Dalkipbi	:	CAC'I'TGGTGGGGC	CANTEGE	CTTATCTA A C	דונבונסטבונטדו. דעקיענונודענטידי	ACCATCATTT	CGTACTTT	:	420
Dalkipb2	:	CACTIGGTGGGGC						:	420
	-	CACTTGGTGGGGC	CAAICGC	CTTATCTAAC	TATADDIADIT		CGTACTT	:	420
DaIRIPb4	:	CWC11GG1GGGC	Cun r CCC					٠	-50
		*	440	*					
DaIRIPb1		AAATAAAACTCCC		ACAAAAAAA	AA : 432				
DaIRIPb2	:	AAATAAAACTCCC							
DaIRIPb3	:	AAATAAAACTCCC							
DaIRIPb4	:	AAATAAAACTCCC							
DOTETA	•								

* 20 * 40 * 60

DaIRIPD : QQRCDWKHNTLLRGSDDNAVSGSKHVVSGTHHVVTGDNNAVTRNHNTVSGSHNTVPGSHN : 60

* 80 *

DaIRIPD : TVSGSHNTVSGSHNTVSGSNHIVSGNNKVVT : 91

		*	20	*	40	*	60		
DaIRIPb	:	ACAGCAACGT	TGTGACTGGAAA	CACAACACAC	TATTACGTGG	GAGTGACGAC	AATGCCGT	:	60
D. T. T. T. T.		*	80 AAGCATGTCGTA	*	100	*	120	_	120
DalRIPb	:	AAGTGGTAGC	AAGCATGTCGTA	TCTGGGACCC	ACCATGICGI	AACTGGCGAC	AACAAIGC	:	120
		*	140	*	160	*	180		
DaIRIPb	:	CGTAACAAGG	AACCACAATACC	STATCCGGGA	GCCATAATAC	CGTACCTGGG	AGCCATAA	:	180
		*	200	*	220	*	240		
DaIRIPb	:	TACCGTATCT	GGGAGCCACAAT	ACCGTATCTG	GGAGCCACAA	TACCGTATCT	GGAAGCAA	:	240
		*	260	*	280	*	300		
DaIRIPb	:	CCACATCGTA	TCTGGGAACAAC	AAAGTCGTGA	CATGAGGTTA	ATGATCTTTA	GTGGATTG	:	300
		*	320	*	340	•	360		
DalRIPb	:	TTTCCATCTT	CCCTAACGAAGC	rcatgttcat(GTCCAAGCTA	ATAAGTGTAC	CTCACAGT	:	360
		*	380	*	400	*	420		
DaIRIPb	:	CACTTGGTGG	GGCCAATCGCGT'	ratgtaactt(GATGGATATA	GCATCATTTT	CGTACTTT	:	420
DaIRIPb		አአአጥአአአኦርጥ	440 CCCTTAAAAAAC	* *********	: 452				
Daikild	•	WWWIWWWCT	CCCITAMANANC		: 432				

			*	20	*	40	*	60		
DaIRIPc1	:	AACAATG'	FIGITICCG	GGAACGACAACI	ACCGTCAT	ATCTGGGAACAG	GAACATTG"	rgrei	:	60
DaIRIPc2	:	AACAATG'	PTGTTTCCG	:GG <mark>-</mark> ACGACAAC <i>i</i>	ACCGTCAT.	ATCTGGGAACAG	GAACATTGT	GTCT	:	59
		· · · · · · · · · · · · · · · · · · ·								
			_		_					
_ ****			*	80	*	100	*	120		
DaIRIPc1	:					TACCATAACCGG			•	120
DaIRIPc2	:	GGGAGCTY	ACAACACCC	TCGTAACTGGG	AGTGATAA	TACCATAACCGG:	INGCAACCA	TGTC	:	119
			*	140	*	160	*	180		
DaIRIPc1	:	GTGTCTG	GGAAGAACC	ATATCGTAACC	BACAACAA	CAACGCCGTAAC	CGGGCACGA	ACAAT	:	180
DaIRIPc2	:	GTGTCTG	GGAAGAACC	'A'TATCGTAACC	GACAACAA	CAACGCCGTAAC	CGGGCACGA	ACAAT	:	179
							_			
			•				•			
			*	200	*	220	*	240		
DaIRIPc1	:					CCACAACACAGT			:	240
DaIRIPc2	;	AATGTAT	CCGGGAGCI	"I'CCA'I'ACCGTA'	I'CCGGGAA	CCACAACACAGT	ATCTGGGA	CAAT	=	239
			•	260	*	280	*	300		
DaIRIPc1		AATGCTG	гатсасісса		STETCCES	GAGCAACAAAGT	CGTGACAGO		•	300
DaIRIPc2	:					GAGCAACAAAGT			:	299
Duna vi	•								_	
			*	320	*	340	*	360		
DaIRIPc1	:					CTAAAGGAGATC			:	360
DaIRIPc2	:	TAATGATA	ATGTCCCTC	CAGGATGCTTCC	CATGTTCC	CTAAAGGAGATC	GCGGCATTO	TACA	:	359
			*	380	*	400	*	420		
DaIRIPc1		AGTTTTTTC	гатасстсь		rgggacc'a	ATCGCGATGTCA	- PGTAACTTO		•	420
DalRIPc2	:					ATCGCGATGTCA'			:	419
Danai vz	٠								•	
			*	440	*	460	*			
DaIRIPc1	:					CCTTGTGGAAAA	AAAAAA	473		
DaIRIPc2	:	ATATAGC	ATCCTTTTC	'CTAATTTAAA'I'	AAAGTTTG	NCTTGTGGA ~	:	463		

* 20 * 40 * 60
DaIRIPC: NNVVSGNDNTVISGNRNIVSGSYNTVVTGSDNTITGSNHVVSGKNHIVTDNNNAVTGHDN: 60

* 80 * 100
DaIRIPC: NVSGSFHTVSGNHNTVSGSNHVVSGSNKVVTGG: 100

		-	20		40	-	90		
DaIRIPC	:	AACAATGTTGTTTC	CCGGGAACGAC	AACACCGT	CATATCTGGG.	AACAGGAACAI	TGTGTCT	:	60
DaIRIPc	:	GGGAGCTACAACAC	80 CCGTCGTAACT	* GGGAGTGA	100 TAATACCATA	* ACCGGTAGCAA	120 CCATGTC	:	120
DaIRIPc	:	÷ GTGTCTGGGAAGAI	140 ACCATATCGTA	* ACCGACAA	160 CAACAACGCC	* GTAACCGGGCA	180 CGACAAT	:	180
		*	200	*	220	*	240		
DaIRIPc	:	AATGTATCCGGGA	CTTCCATACC	GTATCCGG	GAACCACAAC.	ACAGTATCTGG	GAGCAAT	:	240
DaIRIPc ,	:	* AATGCTGTATCAGG	260 GGAGCAACCAI	* CGTCGTGTC	280 CGGGAGCAAC	* AAAGTCGTGAC	300 CAGGAGGT	:	300
DaIRIPc	:	* TAATGATATGTCCC	320 STGCAGGATGC	* TTCCATGT	340 TCCCTAAAGG	* AGATÇGCGGCA	360 ATTGTACA	:	360
DaIRIPc	:	* AGTTTTGTGTAGC	380 CACAATCACT	* TGGTGGGA	400 CCAATCGCGA	* IGTCATGTAAC	420 ETTCATGG	:	420
DaIRIPc	:	* ATATAGCATCCTT	440 PTCCTAATTTA	* LDAKATAAA	460 TTGCCTTGTG	* ************************************	473		

DaIRIPd	:	* 20 * 40 * 60 GACAACACTTGCGAATCACTTGCATTCCAAAAAAGTCCATTCCTGAGTTGCATACCACAG:	60
DaIRIPd	:	* 80 * 100 * 120 CTGAATCCATGGCGCCGCGTGGTCCGGCGCCTCATGCTGCGACTGGGAAGGCGTGAGCAT : :	120
DaIRIPd	:	* 140 * 160 * 180 CCTTGGCGGGCCTCACGCGGCATGTGAAAGGTAACAGGAGAACACTTGCCGTACAACCGA : :	180
DaIRIPd	:	* 200 * 220 * 240 ATACAATTACTGGGACCAACAACGTCAGGTCTGGGAGCAACAATGTTGTTTCCGGGA :	240
DaIRIPđ	:	* 260 * 280 * 300 ACGACAACACCGTCATATCTGGGAACAGGAACATTGTGTCTGGGAGCTACAACACCGTCG :	300
DaIRIPd	:	* 320 * 340 * 360 TAACTGGGAGTGATAATACCATAACCGGTAGCAACCATGTCGTGTCTGGGAAGAACCATA :	360
DaIRIPd	=	* 380 * 400 * 420 TCGTAACCGACAACAACAACGCCGTAACCGGGCACGACAATAATGTATCCGGGAGCTTCC :	420
DaIRIPd	:	* 440 * 460 * 480 ATACCGTATCCGGGAACCACAACACAGTATCTGGGAGCAATAATACTGTATCAGGGAGCA :	480
DaIRIPd	=	* 500 * 520 * 540 ACCATGTCGTGTCCGGGAGCAACAAAGTCGTGACAGGAGGTTAATGATATGTCCGTGCAG :	540
DaIRIPd	:	* 560 * 580 * 600 GATGCTTCCATGTTCCCTAAAGGAGATCGCGGCATTGTACAAGTTTTGTGTAGCTCACAA :	600
DaIRIPd	:	* 620 * 640 * 660 TCACTTGGTGGGACCAATCGCGATGTCATGTAACTTCATGGATATAGCATCCTTTTCCTA:	660
Datripd		* 680 * ATTTAAATAAAGTTTGCCTTGTGTAAAAAAAAAA : 695	

* 20 * 40 * 60

Dairipd: AslagltrhvkgnrrtlavQpntitgtnnnvrsgsnnvvsgndntvisgnrnivsgsynt: 60

* 80 * 100 * 120

DaIRIPd: VVTGSDNTITGSNHVVSGKNHIVTDNNNAVTGHDNNVSGSFHTVSGNHNTVSGSNNTVSG :120

DaIRIPd : SNHVVSGSNKVVTGG : 135

		*	20		*	40		*	60		
DaIRIPel		CGATTAAGCA	GTGGTAAC	AACGCAG	AGTACGO	GGGGAG-C	CCAAGGA	ACACTT	ACGAATCAC	:	60
DaIRIPe2	:					GA(CAAGGA	ACACTT	ACGAATCAC	:	24
	:								ACGAATCAC		23
DaIRIPe3	:						G - 13/C/C/21	MCMCII	veaureve	•	~~
		*	80		*	100		*	120		
DaIRIPel	:	TTGCATTCCA	AAGAAGGT	TTCTTAC	TCAGTTO	TTGCGTCT	TGTGTAT	GCATAG	CGTAACACA	:	121
DaIRIPe2		TTGCATTCCA	AAGAAGGT	TTCTTAC'	TCAGTTG	TTGCGTCT	TATETE	GCATAG	CGTAACACA	:	85
DaIRIPe3	:	TTGCATTCCA	ANGANGGT	יינויט בינוייט ערי	телетте	יייהכיהייי	TATET	GCATAG	CGTAACACA	:	84
Darktee	:	TIGCALICCA	MAGMMCCI	IICIINC	TCFICTIC	,11000.01				-	-
									180		
		* *	140		*	160					202
DaIRIPe1	:	GCTTGAGTCC	:ATGGCGAA	CTCCTCT	C'I'GC'I'AC	TCCTCTTC	TTTGGCG	CTACTC	TIGCCIGCG	:	182
DaIRIPe2	:	GCTTGAGTCC	'ATGCCGAA	CTCCTGT	CTGCTAC	TCCTCTTC	CTTGGCG	CTACTC	TTGCCTGCG	:	146
DaIRIPe3	:	GCTTGAGTCC	CATGGCGAA	CTGCTGT	CTGCTAC	TCCTCTTC	CTTGGCG	CTACTC	TTGCCTGCG	:	145
		*	200	*		220	*		240		
DaIRIPe1		GCTGGGAAGC	CCTCCCC	CCGACAG	CGCAAGO	'GGCCGCG'	CACGGC	GATGTT	GCTCCCCAG	:	243
	•	GCTGGGAAGG		CCCACAC	CCCDAGG	יפפררפרפי	CACGGC	GATGTT	GCTCCCCAG	:	207
DaIRIPe2	:	GCTGGGAAGG		CCCACAG	CCCNACC			CATCTT	CCTCCCAG	:	206
DaIRIPe3	:	GCTGGGAAGG		GCGMCMG.		.660066	2022000	GNIGII	derecene	•	200
								_			
		*	260	*		280	*		00		
DaIRIPe1	:	GCACGGCCTC	CGCGAAGCC	CGTCCCA	GGAGCAT	CCTTGGC	SAGCCTC	GCACGG	CTAGAGGAG	÷	304
DaIRIPe2	:	GCACGGCCTC	CGCGAAGCC	CGTCCCA:	GGAGCA'	CCTTGGC	GAGCCTC	GCACGE	CTAGAGGAG	:	268
DaIRIPe3	:	GCACGGCC1'C	CGCGAAGCC	CCTCCCA	CGACCAT	CCTTGGC	SAGCCTC	GCACGG	CTAGAGGAG	:	267
		*	320	*	34	10	*	36	0		
DaIRIPel		CTCTTCAAGO	CTAACAGA	AGAACAC			ATACAA	TTCAAG	GGACCAACA	:	365
	•	CTCTTCAAGC		אכים אכיים כ	TOCACC!	ACACICCA	4474'04	ם ב שיוי יר	GGACCAACA	:	329
DaIRIPe2	:	CTCTTCAAGC		MOMMENE	10024001	ACACCCA!	מ מכאבונו	מארויידי	CCACCAACA	:	328
DaIRIPe3	:	CTCTTCAAGC	GIAACAGA	MGAACAC	IUUAGG	MCMGCCA	AR I AC AA	TICHE	doncer in terr	•	220
		_				_		400			
		* 3	380	· ·	400		,, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	420		_	426
DaIRIPe1	:	ACAATGTCAC	GAGATGGGT	GCTACAA	TGCTCT.	rTCTGGAA/	ATGACAA	CACTGI	CATATCUGG	:	426
DaIRIPe2	:	ACAATGTCAG	SAGATGCGT	rgc'i'acaa	TGCTCT	FTCTCGAA	ATGACAA	CACTGI	CATATCCGG	:	390
DaIRIPe3	:	ACAATGTCAC	BAGATGGGT	GCTACAA	TGCTCT:	TCTGGAA	ATGACAA	.CACTGI	CATATCCGG	:	389
		* 44	10	*	460		*	480			
DaIRIPel	•	AAACAACAA	CACTGTGTC	TGGGAGC	TTTAAC	ACTATCGT/	AACTGGG	TGTCAC	ANCACTGTG	:	487
DaIRIPe2	:	AAACAACAAG	ACTGTGTC	"TGGGAGC	TTTAAC	CTATCGT	AACTGGG	TGTCAC	AACACTG1G	:	451
DaIRIPe3	:	AAACAACAA	тастстстст	TEGGAGO	ΤΤΤΆΑΟ	CTATCGT	AACTGGG	TGTCAC	AACACTGTG	:	450
つなすどすを合う	٠										
								•			
			n	*	520	,	*	540			
		* 500 TCTGGTAGC/		nemenae			CTA A CTC		ACAATGACG		548
DaIRIPe1	:	TCTGGTAGC/	W.CCV.GGII		GGCTCA	ACCMINIC			אכאה וטהכט	:	512
DaIRIPe2	:	TCTGGTAGC/	MCCAGGT	GREACCE	GGCTCA	*CCATATC		A CONCA	7 C 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		
DaIRIPe3	:	TCTGGTANC	AACCAGGT"	relience	GGC,T,C,V	ICCATATC	2 I MICTO	ACGACA	ACAA I GACG	:	511

	*	560	*	580	*	600			
DaIRIPe1	:						GAGCCACAATAC	-	609
DaIRIPe2	:	TATCAGGTAA	CGATAATAA	CTATCCGGT/	AGCTTTCATA	CCGTATCTG	GAGCCACAATAC	-	573
DaIRIPe3	:	TATCAGGTAA	CGATAATAAT	rgTatccggt/	AGCTTTCATA	CCGTATCTGC	GACCCACAATAC	:	572
DaIRIPel		620	*	640	* 	660	* GGGAGTAACAAA		670
Dalkipei Dalkipe2	•	CGIAICIGG	143C444C4411	ACCOINTCIO	CACAAAACCA	TGTCGTAACT	GGGAGTAACAAA	•	634
Dalkipez Dalkipe3	•	CGTATCTGGG				Nei Comme			610
Darkires	•	680	*	700	*	720	*	٠	
DaIRIPel	_		יכיא פפייידא איזי		ייבור א חייוניתיייזי		TAACGAAGC'I'I.A	•	731
DaIRIPe1	•	CHCCHCACAC	CACGIIAMI	ant charters	COMPTETT			•	_
Dalkipe2 Dalkipe3	•							•	_
	•	740	*	760	*	780	*		
DaIRIPel	:	CGCCCTTGTC	CAAGTTCAA	CCTAGAGCTC	ACAATATCTT	GGTGGGGCCZ	ATCGTCTTATGT	:	792
DaIRIPe2	:							:	-
DaIRIPe3	:							•	-
		800	*	820	*	840	*		
DaIRIPel	:	AACTTCATGC	SATGTATCCT	CCTTTTCCTA	AATAAATTT	ATTTCCTTA	AATGTCTTCCAA	:	853
DaIRIPe2	:							:	-
DaIRIPe3	:							:	-
		860							
DaIRIPe1	:	AAAAAAA	: 862						
DaIRIPe2	:		: -						
DaIRIPe3	:		: -						

FIGURE 11 (cont..)

* 20 * 40 * 60

DaIRIPE : MLLPRHGLAKPVPGASLASLARLEELFKRNRRTLEEQPNTIQGTNNNVRDGCYNALSGND : 60

* 80 * 100 * 120

DaIRIPE : NTVISGNNNTVSGSFNTIVTGCHNTVSGSNQVVSGLNHIVTDDNNDVSGNDNNVSGSFHT :120

* 140 *

DaIRIPE : VSGSHNTVSGSNNTVSGRNHVVTGSNKVVTGG : 152

DaIRIPe	:	CGATTAAC		20 AACAACGCAGAG	* FTACGCGGG	40 GAGACCAAGGA	* ACACTTACG/	60 AATCA	:	60
DaIRIPe	:	CTTGCAT	* PCCAAAGA	80 AGGTTTCTTACI	* CAGTTGTT	100 GCGTCTGTGTA		L20 TAACA	:	120
DaIRIPe	:	CAGCTTG		140 GCGAACTGCTGI	* CCTGCTACT	160 CCTCTTCTTGG		180 IGCCT	:	180
DaIRIPe	:	GCGGCTG		200 TGGGCTGCGACA	* \GCGCAAGC	220 GGCCGCGTCAC		240 SCTCC	:	240
DaIRIPe	:	CCAGGCAG		260 CGAAGCCCGTCC	* CCAGGAGCA	280 TCCTTGGCGAG		300 GCTAG	:	300
DaIRIPe	:	AGGAGCT	* CTTCAAGO	320 GTAACAGAAGA	* ACACTGGAG	340 GAACAGCCAAA		360 AGGGA	:	360
DaIRIPe	:	CCAACAA	* CAATGTCA	380 .GAGATGGGTGC	* FACAATGCT	400 CTTTCTGGAAA		420 IGTCA	:	420
DaIRIPe	:	TATCCGG	* AAACAACA	440 ACACTGTGTCTC	* GGAGCTTT	460 'AACACTATCGT		480 ICACA	:	480
DaIRIPe	:	ACACTGT	* GTCTGGTA	500 GCAACCAGGTT(* STGTCCGGG	520 CTCAACCATAT		540 CGACA	:	540
DaIRIPe	:	ACAATGA	* CGTATCAG	560 GTAACGATAATA	* \ATGTATCO	580 GGTAGCTTTCA		600 IGGGA	:	600
DaIRIPe	:	GCCACAA'	* TACCGTAI	620 CCTGGGAGCAACA	* \ATACCGTA	640 ATCTGGGAGAAA		660 AACTG	:	660
DaIRIPe	:	GGAGTAA	* CAAAGTCG	680 FIGACAGGAGGT	* PAATGATCA	700 AGTGAGTGGATT		720 TTCAC	:	720
DaIRIPe	:	TAACGAA	* GCTTACGO	740 CCTTGTCCAAG	* ITCAACCTA	760 AGAGCTCACAAT		780 GGGCC	:	780
DaIRIPe	:	AATCGTC	* TTATGTAF	800 ACTTCATGGATG	* PATCCTCC1	620 PTTTCCTACTTT		840 TCCTT	ï	840
DaIRIPe	:	AAAATGT	* CTTCCAA	860 AAAAAAAA : :	B <i>6</i> 3					

		*		20	*	40	*	60		
DaIRIPf1		CCCCAGGC	GCGGCC'I'	CCCCCCCAT	CACACGAC	CAACCTTGGCC	GGCCTGACA	CGGCT	:	60
DaIRIPf2	:	@CCCAGGG	CCCC-CT	CCCCCC-CCCA	I'CA CAGGAC	SC-A-CTTGGCC	GGCCTGACA	CCCCT	:	56
	•	GCCC440GC	CCCCPCI		TONCHOUSE	CAACCTTGGCC	CCCCTCACA	CCCCT	:	60
DaIRIP£3	:	CCCCAGGC	GCGGCCT	LULUGGULUCA.		SCALLCT IGGCC	GOCCIONCA	100001	•	00
		*		80	*	100	*	120		
DaIRIPf1	:	TGAGTCGC	TCAACCT	TGCCANCAACAC	TCTGGTAC	GCACCATCCCA	TCNTGGATC	GGTGA	:	120
DaIRIPf2	•	TGAGTCGC	TCAACCT	TGCCAACACAC	TCTGGTAC	GCACCATCCCA	TCATGGATC	CGTGA	:	116
DaIRIPf3	•	TCACTCCC		TGCCAACAACA	PALEGUAG	GCACCATCCCA	TCATGGATC	GGTGA	:	120
Dalkifla	•	TOMOTOGO	ICHICCI	100cmicrii-ce	0100111					
		*		140	*	160	r	180		
DaIRIPfl	:	GCTTGACC	NCCTTTG	CTACATGGATC:	I'CTCACAC!	\ATTCACTAGAT	GGCGAGG'I'A	CCCAA		180
DaIRIPf2	:	GCTTGACC	ACCTTTG	CTACATGGATC:	TCTCACAC <i>I</i>	\ATTCACTAGAT	GGCGAGGT	ACCCAA	:	176
DaIRIPf3	:	GCTTGACC	ACCTTTG	CTACATGGATC	TCTCACAC	\ATTCACTAGAT	GGCGAGGTA	CCCAA	:	180
		•		200	*	220	*	240		
D-707D51		G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3			TCACTACO1	ACCEGTCGTTCA	CTCCCCATC		٠	240
DaIRIPfl	•	GAGTTTGC	AGATACG	CCICAGOGCCC.			CIGOCCAIC		:	236
DaIRIP£2	:	GAGTTTEGC	AGATACG	GCTCAGGGCCC.	TCACTACGA	ACCGGTCGTTCA	CIGGGCAIG		•	
DaIRIPf3	:	GAGTTTGC	AGATACG	GCTCAGGGCCC'	I'CACTACG/	ACCGGTCGTTCA	CTGGGCATG	Giral	:	240
		*		260	*	280	*	300		
DaIRIPfl		CATTAACA			GTAGCCGAZ	AGAACACTCCAA	GAACAACCA	LAATGT	:	300
	•	CATINAACA	TOCCCTT TOCCCTT	CCATATCAACC	CTACCCCA?	AGAACACTCCAA	GAACAACCI	TOTAA	:	296
DaIRIPf2	:	CALIAACA	TGCCGII	GCMIMIGN MAC	GIAGCCCA1	AGAACACTCCAA	CARCARCCI	AATCT	:	300
DaIRIPf3	:	CATTAACA	TGCCGTT	GCATATGAAGC	IN AGCCGAZ	AGMACAC I CCAA		VALUE OF L	•	300
		*		320	*	340	*	360		
DaIRIPf1	:	* AATAACTC	GGACCAA	CAACAGTGTCA	* GATCTGGG/	AGAAACAATGTT	* GTTTCCGGG	AACGA		360
	:	AATAACTG	GGACCAA	CAACAGTGTCAG CAACAGTGTCAG	GATCTGGG!	AGAAACAATGTT AGAAACAATGTT	GTTTCCGGG	AACGA AACGA		360 356
DaIRIPf2	:	AATAACTG	GGACCAA	CAACAGTGTCAG CAACAGTGTCAG	GATCTGGG!	AGAAACAATGTT AGAAACAATGTT	GTTTCCGGG	AACGA AACGA		
	: :	AATAACTG	GGACCAA	CAACAGTGTCAG CAACAGTGTCAG	GATCTGGG!	AGAAACAATGTT	GTTTCCGGG	AACGA AACGA	:	356
DaIRIPf2	: :	AATAACTG	GGACCAA	CAACAGTGTCAG CAACAGTGTCAG	GATCTGGG!	AGAAACAATGTT AGAAACAATGTT	GTTTCCGGG	AACGA AACGA	:	356
DaIRIPf2	: :	AATAACTG	IGGACCAA IGGACCAA IGGACCAA	CANCAGTGTCA(CANCAGTGTCA(CANCAGTGTCA(GATCTGGG!	AGAAACAATGTT AGAAACAATGTT AGAAACAATGTT	GTTTCCGGG	BAACGA BAACGA BAACGA	:	356
DaIRIPf2 DaIRIPf3	:	DTDAATAA DTDAATAA *	IGGACCAA IGGACCAA IGGACCAA	CANCAGTGTCA: CANCAGTGTCA: CANCAGTGTCA: 380	GATCTGGGA GATCTGGGA *	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT	GTTTCCGGG GTTTCCGGG	GAACGA GAACGA GAACGA	:	356 360
DaIRIPf2 DaIRIPf3 DaIRIPf1	: :	AATAACTG AATAACTG * CAATACTG	GGACCAA GGACCAA GGACCAA	CAACAGTGTCA CAACAGTGTCA CAACAGTGTCA 380 TGGGAACAACA	GATCTGGGA GATCTGGGA * ATGTTGTGT	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC	GTTTCCGGG GTTTCCGGG * AACACTGTC	EAACGA EAACGA EAACGA 420 EGTAAC	:	356 360 420
DaIRIPf2 DaIRIPf3 . DaIRIPf1 DaIRIPf2	: : :	AATAACTG AATAACTG * CAATACTG CAATACTG	GGACCAA EGGACCAA EGGACCAA EGGACCAA ETCATATC	CAACAGTGTCA CAACAGTGTCA CAACAGTGTCA 380 TGGGAACAACA TGGGAACAACA	GATCTGGGA GATCTGGGA * ATGTTGTG ATGTTGTG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 TCTGGGAGCCAC	GTTTCCGGG GTTTCCGGG * AACACTGTC	AACGA AACGA AACGA A20 CGTAAC	:	356 360 420 416
DaIRIPf2 DaIRIPf3 DaIRIPf1	: : : : : : : : : : : : : : : : : : : :	AATAACTG AATAACTG * CAATACTG CAATACTG	GGACCAA EGGACCAA EGGACCAA EGGACCAA ETCATATC	CAACAGTGTCA CAACAGTGTCA CAACAGTGTCA 380 TGGGAACAACA TGGGAACAACA	GATCTGGGA GATCTGGGA * ATGTTGTG ATGTTGTG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC	GTTTCCGGG GTTTCCGGG * AACACTGTC	AACGA AACGA AACGA A20 CGTAAC	:	356 360 420
DaIRIPf2 DaIRIPf3 . DaIRIPf1 DaIRIPf2	: : : : : : : : : : : : : : : : : : : :	AATAACTG AATAACTG * CAATACTG CAATACTG	GGACCAA EGGACCAA EGGACCAA EGGACCAA ETCATATC	CAACAGTGTCA CAACAGTGTCA CAACAGTGTCA 380 TGGGAACAACA TGGGAACAACA	GATCTGGGA GATCTGGGA * ATGTTGTG ATGTTGTG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 TCTGGGAGCCAC	GTTTCCGGG GTTTCCGGG * AACACTGTC	AACGA AACGA AACGA A20 CGTAAC	:	356 360 420 416
DaIRIPf2 DaIRIPf3 . DaIRIPf1 DaIRIPf2	: : : : : : : : : : : : : : : : : : : :	AATAACTG AATAACTG * CAATACTG CAATACTG	GGACCAA EGGACCAA EGGACCAA EGGACCAA ETCATATC	CAACAGTGTCA CAACAGTGTCA CAACAGTGTCA 380 TGGGAACAACA TGGGAACAACA	GATCTGGGA GATCTGGGA * ATGTTGTG ATGTTGTG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 TCTGGGAGCCAC	GTTTCCGGG GTTTCCGGG * AACACTGTC	EAACGA EAACGA EAACGA GAACGA GTAAC GTAAC	:	356 360 420 416
DaIRIPf2 DaIRIPf3 . DaIRIPf1 DaIRIPf2	: : : : : : : : : : : : : : : : : : : :	AATAACTG AATAACTG * CAATACTG CAATACTG CAATACTG	GACCAA GGACCAA AACCAA ATTATTT TCATATC TCATATC	CAACAGTGTCA CAACAGTGTCA CAACAGTGTCA 380 TGGGAACAACA TGGGAACAACA TGGGAACAACA	GATCTGGGA GATCTGGGA ATGTTGTGT ATGTTGTGT ATGTTGTGT	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 I'CTGGGAGCCAC I'CTGGGAGCCAC I'CTGGGAGCCAC	GTTTCCGGG GTTTCCGGG * AACACTGTC AACACTGTC AACACTGTC	AACGA AACGA AACGA AACGA AACGA AACGA AACGA AACGA AACGA AACGAAC	:	356 360 420 416 420
DaIRIPf2 DaIRIPf3 . DaIRIPf1 DaIRIPf2	: : : : : : : : : : : : : : : : : : : :	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG	GGACCAA GGACCAA AACACACACACACACACACACACA	CAACAGTGTCA CAACAGTGTCA CAACAGTGTCA 380 TGGGAACAACA TGGGAACAACA TGGGAACAACA 440 CGTAAGTGGTA	ATCTGGGA ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 FCTGGGAGCCAC FCTGGGAGCCAC FCTGGGAGCCAC	* AACACTGTC AACACTGTC AACACTGTC AACACTGTC	AROCA BAACGA BAACGA CGTAAC CGTAAC CGTAAC	:	356 360 420 416
DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf3	:::::::::::::::::::::::::::::::::::::::	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG	GGACCAA GGACCAA AACACACACACACACACACACACA	CAACAGTGTCA CAACAGTGTCA CAACAGTGTCA 380 TGGGAACAACA TGGGAACAACA TGGGAACAACA 440 CGTAAGTGGTA	ATCTGGGA ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 FCTGGGAGCCAC FCTGGGAGCCAC FCTGGGAGCCAC	* AACACTGTC AACACTGTC AACACTGTC AACACTGTC	AROCA BAACGA BAACGA CGTAAC CGTAAC CGTAAC		356 360 420 416 420
DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf1	:::::::::::::::::::::::::::::::::::::::	AATAACTG AATAACTG ** CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG	GGACCAA GACCAA GACC	CAACAGTGTCACCAACAGTGTCACCAACAGTGTCACAACACACAC	ATCTGGGA ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT TANCCATG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC	# AACACTGTC AACACTGTC AACACTGTC AACACTGTC ACCAACCAT	A 80 FOTCGT		356 360 420 416 420
DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf3	:::::::::::::::::::::::::::::::::::::::	AATAACTG AATAACTG ** CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG	GGACCAA GACCAA GACC	CAACAGTGTCACCAACAGTGTCACCAACAGTGTCACAACACACAC	ATCTGGGA ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT TANCCATG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 FCTGGGAGCCAC FCTGGGAGCCAC FCTGGGAGCCAC	# AACACTGTC AACACTGTC AACACTGTC AACACTGTC ACCAACCAT	A 80 FOTCGT	: : : : : : : : : : : : : : : : : : : :	356 360 420 416 420 480 476
DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf1	:::::::::::::::::::::::::::::::::::::::	AATAACTG AATAACTG ** CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG	GGACCAA GACCAA GACC	CAACAGTGTCACCAACAGTGTCACCAACAGTGTCACAACACACAC	ATCTGGGA ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT TANCCATG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC	# AACACTGTC AACACTGTC AACACTGTC AACACTGTC ACCAACCAT	A 80 FOTCGT	: : : : : : : : : : : : : : : : : : : :	356 360 420 416 420 480 476
DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf1	:::::::::::::::::::::::::::::::::::::::	AATAACTG AATAACTG ** CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG	GGACCAA GACCAA GACC	CAACAGTGTCAC CAACAGTGTCAC CAACAGTGTCAC 380 TGGGAACAACA TGCGAACAACA TGCGAACAACA CGTAAGTGGTAC CGTAAGTGGTAC	ATCTGGGA ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT ATGTTGTGT TANCCATG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 TCTGGGAGCCAC TCTGGGAGCCAC TCTGGGAGCCAC 460 ETCGTATCTAGG ETCGTATCTAGG	# AACACTGTC AACACTGTC AACACTGTC AACACTGTC ACCAACCAT	A20 GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC	: : : : : : : : : : : : : : : : : : : :	356 360 420 416 420 480 476
DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3	:	AATAACTG AATAACTG CAATACTG **	GGACCAA GGACCAA GGACCAA TCATATC TCATATC TCATATC ACAATGT ACAATGT	CAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGGGAACAACAACAGTGGGAACAACAACAGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAACGGTAAGTGGTAA	* ATGTTGTG ATGTTGTG ATGTTGTG ATGTTGTG TGTAACCAT GTAACCAT	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC	* AACACTGTC AACACTGTC AACACTGTC * ACCAACCAT ACCAACCAT	ARACGA ARACCA ARACGA ARACCA AR	: : : : : : : : : : : : : : : : : : : :	356 360 420 416 420 480 476 480
DaIRIPf1 DaIRIPf1 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1	:	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG GGGGAGTG AACTGATA	GGACCAA	CAACAGTGTCAM CAACAGTGTCAM CAACAGTGTCAM 380 TGGGAACAACAM TGGGAACAACAM 440 CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM	* ATGTTGTGT ATGTTGTGT ATGTTGTGT * GTANCCATC GTANCCATC	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC 460 ETCGTATCTAGG ETCGTATCTAGG ETCGTATCTAGG	# AACACTGTC AACACTGTC AACACTGTC ACCAACCAT ACCAACCAT ACCAACCAT ACCAACCA	A20 GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC	***	356 360 420 416 420 480 476 480
DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3	:	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG GGGGAGTG AACTGATA	GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GACAACAA	CAACAGTGTCAM CAACAGTGTCAM CAACAGTGTCAM 380 TGGGAACAACAM TGGGAACAACAM TGCGAACAACAM 440 CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM	# ATGTTGTGT ATGTTGTGT ATGTTGTGT # GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC A60 ETCGTATCTAGG ETCGTATCTAGG ETCGTATCTAGG ETCGTATCTAGG	# AACACTGTC AACACTGTC AACACCAT ACCAACCAT ACCAACCAT ACCAACCA	A20 GTAAC		356 360 420 416 420 480 476 480 540 536
DaIRIPf1 DaIRIPf1 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1	:	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG GGGGAGTG AACTGATA	GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GACAACAA	CAACAGTGTCAM CAACAGTGTCAM CAACAGTGTCAM 380 TGGGAACAACAM TGGGAACAACAM TGCGAACAACAM 440 CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM	# ATGTTGTGT ATGTTGTGT ATGTTGTGT # GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC 460 ETCGTATCTAGG ETCGTATCTAGG ETCGTATCTAGG	# AACACTGTC AACACTGTC AACACCAT ACCAACCAT ACCAACCAT ACCAACCA	A20 GTAAC	***	356 360 420 416 420 480 476 480 540 536
DaIRIPf2 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf1	:	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG GGGGAGTG AACTGATA	GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GACAACAA	CAACAGTGTCAM CAACAGTGTCAM CAACAGTGTCAM 380 TGGGAACAACAM TGGGAACAACAM TGCGAACAACAM 440 CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM	# ATGTTGTGT ATGTTGTGT ATGTTGTGT # GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC A60 ETCGTATCTAGG ETCGTATCTAGG ETCGTATCTAGG ETCGTATCTAGG	# AACACTGTC AACACTGTC AACACCAT ACCAACCAT ACCAACCAT ACCAACCA	A20 GTAAC		356 360 420 416 420 480 476 480 540 536
DaIRIPf2 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf1	:	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG GGGGAGTG AACTGATA	GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GACAACAA	CAACAGTGTCAM CAACAGTGTCAM CAACAGTGTCAM 380 TGGGAACAACAM TGGGAACAACAM TGCGAACAACAM 440 CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM CGTAAGTGGTAM	# ATGTTGTGT ATGTTGTGT ATGTTGTGT # GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG GTANCCATG	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC A60 ETCGTATCTAGG ETCGTATCTAGG ETCGTATCTAGG ETCGTATCTAGG	# AACACTGTC AACACTGTC AACACCAT ACCAACCAT ACCAACCAT ACCAACCA	A20 GTAAC		356 360 420 416 420 480 476 480 540 536
DaIRIPf2 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf1	:	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG CAATACTG CAATACTG AACTGATA AACTGATA AACTGATA AACTGATA	GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GCAATGT GACAATGT GACAATGT	CAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGGTAACAGTGGTAACGGTAACGGTAACGGTAACGGTAACCGTAACGGTAACCGTAACCGTAACCGTAACCGTACCGTAACCGTAACCGTAACCGTAACCGTAACCGTAACCGGTAACCGGTAACCGGTAACCGGTAACCGGTAACCGGTAACCGGTAACCGGTAACCG	* ATCTTGGG ATCTTGTGT ATGTTGTGT ATGTTGTGT TAACCATC GTAACCATC GGAACCACC GGAACCACC	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 TCTGGGAGCCAC TCTGGGAGCCAC TCTGGGAGCCAC TCTGGTATCTAGG TCGTATCTAGG TCGTATCTAGG TCGTATCTAGG AACACTGTATCC	* AACACTGTC AACACTGTC AACACTGTC AACACCATGTC ACCAACCAT ACCAACCAT ACCAACCAT ACCAACCA	420 GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTCGT GTCGT GTCGT GTCGT GTCGT GTCGT GTCGT		356 360 420 416 420 480 476 480 540 536
DaIRIPf2 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf3	: : : : : : : : : : : : : : : : : : : :	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG CAATACTG CAATACTG AACTGATA AACTGATA AACTGATA AACTGATA	GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GCAATGT GACAATGT GACAATGT	CAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGGTAACAGTGGTAACGGTAACGGTAACGGTAACGGTAACCGTAACGGTAACCGTAACCGTAACCGTAACCGTACCGTAACCGTAACCGTAACCGTAACCGTAACCGTAACCGGTAACCGGTAACCGGTAACCGGTAACCGGTAACCGGTAACCGGTAACCGGTAACCG	* ATCTTGGG ATCTTGTGT ATGTTGTGT ATGTTGTGT TAACCATC GTAACCATC GGAACCACC GGAACCACC	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 TCTGGGAGCCAC TCTGGGAGCCAC TCTGGGAGCCAC TCTGGTATCTAGG TCGTATCTAGG TCGTATCTAGG TCGTATCTAGG AACACTGTATCC	* AACACTGTC AACACTGTC AACACTGTC AACACCATGTC ACCAACCAT ACCAACCAT ACCAACCAT ACCAACCA	420 GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTCGT GTCGT GTCGT GTCGT GTCGT GTCGT GTCGT		356 360 420 416 420 480 476 480 540 536
DaIRIPf1 DaIRIPf3 DaIRIPf1 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf1 DaIRIPf1 DaIRIPf1 DaIRIPf1 DaIRIPf3	: : : : : : : : : : : : : : : : : : : :	AATAACTG AATAACTG CAATACTG CAATACTG CAATACTG CAATACTG CAATACTG CAATACTG AACTGATA AACTGATA AACTGATA AACTGATA AACTGATA	GGACCAA GGACCAA GGACCAA GGACCAA GCAATGT GACAATGT GACAACGA ACAACAA ACAACAA	CAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACACAACAACAACAACAACAACAACAACAACAACAAC	* ATCTTGGG ATGTTGTG ATGTTGTG ATGTTGTG ATGTTGTG * GTAACCATC GTAACCATC GGAACCACC GGAACCACC GGAACCACC CCGGGAGC * CCGGGAGC	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC ICTGGGAGCCAC 460 ITCGTATCTAGG ITCGTATCTAGG ICGTATCTAGG ACACTGTATCC AACACTGTATCC AACACTGTATCC AACACTGTATCC AACACTGTTATCC IS80 AACCATGTTGTA	# AACACTGTO AACACTGTO AACACTGTO AACACTGTO ACCAACCAT ACCAACCAT ACCAACCAT ACCAACCAT ACCAACCA	420 GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTCGT GTCGT GTCGT GTCGT GTCGT		356 360 420 416 420 480 476 480 540 536
DaIRIPf2 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf1 DaIRIPf2 DaIRIPf3 DaIRIPf3 DaIRIPf1 DaIRIPf3	: : : : : : : : : : : : : : : : : : : :	AATAACTG AATACTG CAATACTG CAATACTG CAATACTG CAATACTG GGGGAGTG GGGGAGTG GGGGAGTG AACTGATA AACTGATA AACTGATA AACTGATA AACTGATA ATGATA ATGATA ATGATA ATGATA	GGACCAA GGACCAA GGACCAA GGACCAA GGACCAA GCAATGT GACAATGT GACAACAA ACAACAA ACAACAA	CAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACAGTGTCAACACACAC	# ATGTTGTG ATGTTGTG ATGTTGTG ATGTTGTG ATGTTGTG # GTAACCATG GTAACCATG GGAACCACA GGAACCACA GGAACCACACACACACAC	AGAACAATGTT AGAAACAATGTT AGAAACAATGTT AGAAACAATGTT 400 TCTGGGAGCCAC TCTGGGAGCCAC TCTGGGAGCCAC TCTGGTATCTAGG TCGTATCTAGG TCGTATCTAGG TCGTATCTAGG AACACTGTATCC	# AACACTGTC AACACTGTC AACACTGTC AACACCAT ACCAACCAT ACCAACCAT ACCAACCA	420 GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTAAC GTCGT GTCGT GTCGT GTCGT GAACAC CAACAC		356 360 420 416 420 480 476 480 540 536 540

			*	620	*	640	*	660	
DaIRIPf1	•	AGTCGTG	ACGGGAGG	TTAATTAATGA'	<u> </u>			:	628
DaIRIPf2	:	AGTCGTC	ACGGGAGG	TTAATTAATGA	TCTATCAGT	GGATTGTCTCC	ATCCTCCCI	CACGC:	656
DaIRIPf3	:	AGTCGTG	ACGGGAGG	TTAATTAATGA'	l'CTA1'CAG'I	GGATTGTCTCC.	ATCGTCCCT	GACGG:	660
			*	680	*	700	*	720	
DaIRIPf1	:							 :	-
DaIRIPf2	:			CCAAGTTCAGT					716
DaIRIPf3	:	AGTTCAC	GTCCTTGT	CCAAGTTCAGT	GTAGCTTAC	AATCACATGGT.	AGGGCCAAT	CGCAT :	720
			*	740	*	760	*	780	
DaIRIPf1								· :	-
Darkieri	٠								
DaIRIPE2	:			ATATAGCATCC				<u></u> ;	742
	:			ATATAGCATCC ATATAGCATCC	TTTTTCTGT	YTTYAAATAA	ACCCCTAAA	CTATC :	742 780
DaIRIPf2	:				ITTTTCTGT	TTAAATAAA	ACCCCTAAA	CTATC :	
DaIRIPf2	:				TTTTTCTGT	TTTAAATAAA	ACCCTAAA	CTATC:	
DaIRIPf2	:				TTTTTCTGT	TTTAAATAAA	ACCCTAAA	CTATC:	
DaIRIPf2	:				FTTTTCTGT	TTTAAATAAA	ACCCCTAAA	ACTATC :	
DaIRIPf2 DaIRIPf3	: :				FTTTTCTGT	TTTAAATAAAA	ACCCTAAA	CTATE:	

FIGURE 14 (cont..)

* 20 * 40 * 60

DaIRIPÉ : MDLSHNSLDGEVPKSLQIRLRALTTTGRSLGMVFINMPLHMKRSRRTLQEQPNVITGTNN : 60

* 80 * 100 * 120

DaIRIPÉ : SVRSGRNNVVSGNDNTVISGNNNVVSGSHNTVVTGSDNVVSGSNHVVSRTNHVVTDNNNA :120

* 140 *

DaIRIPÉ : VTGNHNTVSGSHNTVSGSNNVVSGSNHVVSGSNKVVTGG : 159

DalRipf	:	* CCCCAGGCGCGG	20 CCTCGCGGGC	* CCCATCACAG	40 GAGCAACCT	* rggccggcctga	60 CACGGCT	:	60
DaIRIPf	:	* TGAGTCGCTCAA	80 CCTTGCCAAC	* PAACAGTCTGG	100 FAGGCACCA	* FCCCATCATGGA	120 TCGGTGA	:	120
DaIRIPf	:	* GCTTGACCACCT	140 TTGCTACATG	* GATCTCTCAC	160 ACAATTCAC	* FAGATGGCGAGG	180 TACCCAA	:	180
DaIRIPf	:	* GAGTTTGCAGAT	200 ACGGCTCAGG	* GCCCTCACTA	220 CGACCGGTC	* GTTCACTGGGCA	240 TGGTTTT	:	240
DaIRIPf	:	* CATTAACATGCC	260 GTTGCATATO	* SAAGCGTAGCC	280 Gaagaacac	* CCCAAGAACAAC	300 CAAATGT	:	300
DaIRIPf	:	* AATAACTGGGAC	320 CAACAACAGT	* GTCAGATCTG	340 GGAGAAACA	* ATGTTGTTTCCG	360 GGAACGA	:	360
DaIRIPf	:	* CAATACTGTCAT	380 ATCTGGGAAC	* :AACAATGTTG	400 TGTCTGGGA	* GCCACAACACTG	420 TCGTAAC	:	420
DaIRIPf	ı	* GGGGAGTGACAA	440 TGTCGTAAGT	* GGTAGTAACC.	460 ATGTCGTAT	* CTAGGACCAACC	480 ATGTCGT	:	480
DaIRIPf	:	* AACTGATAACAA	500 CAATGCCGTA	* ACCGGGAACC	520 ACAACACTG	* FATCCGGGAGCC	540 ACAACAC	:	540
DaIRIPf	:	* TGTATCCGGGAG	560 CAACAATGTO	* GTATCCGGGA	580 GCAACCATG	* FTGTATCAGGGA	600 GCAACAA	:	600
DalRIPf	:	* AGTCGTGACGGG	620 AGGTTAATTA	* ATGATCTATC	640 AGTGGATTG	* PCTCCATCGTCC	660 CTGACGG	ı	660
DaIRIPf	:	* AGTTCACGTCCT	680 TGTCCAAGTT	* CAGTGTAGCT	700 TACAATCAC	* ATGGTAGGGCCA	720 ATCGCAT	:	720
Dairipf	:	* TATGTAACTTCA	740 TGGATATAGO	* ATCCTTTTTC	760 TGTTTTAAA	* FAAAAACCCCTA	780 AACTATC	:	780

DaIRIPF : TTACAAAAAAAAA : 795

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